

Figure 1

hDEC2a

DEC1

MDEGIPHLQERQ—L———LEHRDFIGLDYSSLYMC-KPKRSMKRD-DTKDITYKLPHRLIEKKRRDRIN 61

M-ERIPSAQPPPAKAPGLEHGDLPMPAHMYQVYKSRRGIKRSEDSKETYKLPHRLIEKKRRDRIN 69

ECIAQLKDLLPEHLKLTTLGHLEKAVVLELTCLKHLKALTALTEQQHQKIIALQNG———ERSLKSPIQSD 127

ECIAQLKDLLPEHLKLTTLGHLEKAVVLELTCLKHVKALTNLIDQQQKIIALQSGLOAGELSGR-NVETG 138

LDAFHSGFQTCAKEVLQYLSRFESWTPREPRCVQLINHLHAVATQFLTPQLLTQQVPLSKGTGA——PS 194

QEMFCSGFQTCAREVLQYLAKHEN-T-RDLKSSQLVTHLHRVVSSELLQGGTSRKPSDPAPKVMDFKEKPS 206

A-A-GSAAAPCLERAGQKLEPLAYCVPVIQRTQP-SAEAAENDTDTDSGYGGGEAEARPD-R-E———K- 254

SPAKGSEG-P———G-K--N——CVPVIQRTFAHSSGEQSGSDTDTDSGYGGGESEKG-DLRSEQPCFKS 263

—GK—GAGASRVTIKQEPGEDSPAPK-RMKL-DSRGGG-SGGGPGGGAAAAAALLGPDPAAAAAALLR 317

DHGRFTMGERIGAIIKQESE-E-PPTKKNRMQLSDDEGHFTSS—————D————— 305

PDAALLSSLVAFGGGGGAPFP-QAAAAAPFCLPFCFLSP-SAAAAVYQPFLLDKSGLEKYLYPAAAAAPF 385

——LISS—PFLG——PHPHQP———PFCLPF-YLIPPSATA-YL-PML———EKCWYPTSV—P- 349

PLLYPGIPAPAAAAAAAAAAAAAAAAAFCLSSVLSPPPEKAGAAAATLL-PHEVAPLGAPHPQHHPHGRTH 454

VL-YPGLNASAAA—————LSSFMNP-DKISA—PLLMPQR—L—PSP————— 385

LPFAGPREPGNPESSE—QE-DPSQPGK-EA-P 482

LP-AHP———SVDSSVLLQALKPIPLNLETKD

(Homology 43%)

Figure 2

hDEC2a

hDEC2b

MDEGIPHLQERQLLEHRDFIGLDYSSLYMCKPKRSMKRDDTK---DTYKLPRLIEKKRRDRINECIAQLK 68

MDEGIPHLQERQLLEHRDFIGLDYSSLYMCKPKRSMKRDDTKVSDTYKLPRLIEKKRRDRINECIAQLK 70

DLLPEHLKLTTLGHLEKAVVLELTCLKHLKALTALTEQQHQKIIALQNGERSLKSPIQSDLD AFHSGFQTC 138

DLLPEHLKLTTLGHLEKAVVLELTCLKHLKALTALTEQQHQKIIALQNGERSLKSPIQSDLD AFHSGFQTC 140

AKEVLQYLSRFESWTPREPRCVQLINHLHAVATQFLPTPQLLTQQVPLSKGTGAPSAAGSAAAPCLERAG 208

AKEVLQYLSRFESWTPREPRCVQLINHLHAVATQFLPTPQLLTQQVPLSKGTGAPSAAGSAAAPCLERAG 210

QKLEPLAYCVPVIQRTQPSAELAAENDTDTDSGYGGEAEARPDREKKGAGASRVTIKQEPPEGEDSPAPK 278

QKLEPLAYCVPVIQRTQPSAELAAENDTDTDSGYGGEAEARPDREKKGAGASRVTIKQEPPEGEDSPAPK 280

RMKLDSRGGGSGGGPGGGAAAAAALLGPDPAALLLRPDAALLSSLVAFGGGGGAPFPQAAAAAPFC 348

RMKLDSRGGGSGGGPGGGAAAAAALLGPDPAALLLRPDAALLSSLVAFGGGGGAPFPQAAAAAPFC 350

LPFCFLSPSAAAAYVQPFLLDKSGLEKYLPAAPAAAPFLLYPGIPAPAAAAAFAFCLSSV 418

LPFCFLSPSAAAAYVQPFLLDKSGLEKYLPAAPAAAPFLLYPGIPAPAAAAAFAFCLSSV 420

LSPPPEKAGAAAATLLPHEVAPLGAPHPQHGRTHLPFAGPREPGNPESQAQEDPSQPGKEAP 482

LSPPPEKAGAAAATLLPHEVAPLGAPHPQHGRTHLPFAGPREPGNPESQAQEDPSQPGKEAP 484

Figure 3

hDEC2a

mDEC2a

MDEGIPHLQERQLLEHRDFIGLDYSSLYMCKPKRSMKRDDTKDITYKLPHRLIEKKRRDRINECIAQLKDL 70

MDEGIPHLQERQLLEHRDFIGLDYSSLYMCKPKRSLKRDDTKDITYKLPHRLIEKKRRDRINECIAQLKDL 70

LPEHLKLTTLGHLEKAVVLELTCLKHLKALTALTEQQHQKIIALQNGERSLKSPIQSDLD AFHSGFQTC AK 140

LPEHLKLTTLGHLEKAVVLELTCLKHLKALTALTEQQHQKIIALQNGERSLKSPVQADLD AFHSGFQTC AK 140

EVLQYLSRFESWTPREPRCVQLINHLHAVATQFLPTPQLLTQQVPLSK-GTG-AP-SAAGSAAAPCLERA 207

EVLQYLARFESWTPREPRCAQLVSHLHAVATQLL-TPQ-----VP-SGRGSGRAPCSA-G-AAA-----A 196

-GQKLEPLAYCVPVIQRTQPSAELAAENDTDTDSGYGGEAEARPDREKKGAGASRVTIKQEPPGEDS-P 275

SGP-ERVARCVPVIQRTQPGTEP-EHDTDTDSGYGGEAE-QG-R-----A-A-V--KQEPPG-DSSP 249

APKRMKLDSRGGGSGGGPGGGAAAAAALLGPDPAALALRPDAALLSSLVAFGGGGGAPFPQAAAAA 345

APKRPKLEARG-----ALLGPEPA-LL-G-SLVAL-GGGAPFAQAAAA- 288

PFCLPFCFLSPSAAAAYVQPFLDKSGLEKYLPAAPFPLLYPGIPAPAAAAAAAAAAAAAAAAAF PCL 415

PFCLPFYLLSPSAAA-YVQPWLDKSGLDKYLPAAPFPLLYPGIPA-----AAAAAAAAAF PCL 348

SSVLSPPPEKAGA-AAATLLPHEVAPLGAP-HPQHPHGRTHLPFAGPREPGNPRESSAQEDPSQPGKEAP 482

SSVLSPPPEKAGATAGAPFLAHEVAPPG-PLRPQHAHSRTHLPRAV-----NPRESS-QEDATQPAKDAP 410

Figure 4

hDEC2a
mDEC2a
SHARP-1

MDEGIPHLQERQLLEHRDFIGLDYSSLYMCKPKRSMKRODTKDTYKLPRLIEKKRRDRINECIAQLKDL 70
MDEGIPHLQERQLLEHRDFIGLDYSSLYMCKPKRSLKRODTKDTYKLPRLIEKKRRDRINECIAQLKDL 70
MDEGIPHLQERQLLEHRDFIGLDYSSLYMCKPKRSLKRODTKDTYKLPRLIEKKRRDRINECIAQLKDL 70

LPEHLKLTTLGHLEKAVVLELTCLKHLKALTALTEQQHQKIIALQNGERSLKSPIQSDLDAFHSGFQTCAK 140
LPEHLKLTTLGHLEKAVVLELTCLKHLKALTALTEQQHQKIIALQNGERSLKSPVQADLDAFHSGFQTCAK 140
LPEHLKLTTLGHLEKAVVLELTCLKHLKALTALTEQQHQKIIALQNGERSLKSPVQADLDAFHSGFQTCAK 140

EVLQYLSRFESWTPREPRCVQLINHLHAVATQFLTPQLLTQQVPLSK-GTG-AP-SAAGSAAAPCLERA 207
EVLQYLARFESWTPREPRCAQLVSHLHAVATQLL-TPQ-----VP-SGRGSGRAPCSA-G-AAA-----A 196
EVLQYLARFESWTPREPRCAQLVSHLHAVATQLL-TPQ-----VT-PGRGPGRAPCSA-G-AAA-----A 196

-GQKLEPLAYCVPVIQRTQPSAELAAENDTDTDSGYGGEAEARPDREKKGAGASRVTIKQEPPGEDS-P 275
SGP-ERVARCVPVIQRTQPGTEP-EHDTDTDSGYGGEAE-QG-R-----A-A-V-KQEPPG-DSSP 249
SGS-ERVARCVPVIQRTQPGTEP-EHDTDTDSGYGGEAE-QG-R-----A-A-V-KQEPPG-DPSL 249

APKRMKLSRGGGSGGGPGGGAAAAAALLGPDAAAAALLRPDAALLSSLVAFGGGGGAPFPQAAAAA 345
APKRPKLEARG-----ALLGPEPA-LL-G-SLVAL--GGGAPFAQPAAA- 288
RPRG 253

PFCLPFCFLSPSAAAAYVQPFLOKSGLEKYLYPAAAAAPFLLYPGIPAPAAAAAFAFPCL 415
PFCLPFYLLSPSAAA-YVQPWLDKSGLDKYLYPAAAA-PFLLYPGIPA-----AAAAAFAFPCL 348

SSVLSPPPEKAGA-AAATLLPHEVAPLGAP-HPQHPHGRTHLPFAGPREPGNPESSAQEDPSQPGKEAP 482
SSVLSPPPEKAGATAGAPFLAHEVAPPG-PLRPQHAHSRTHLPRAV-----NPES-QEDATQPAKDAP 410